

#4

6/11/02

SEQUENCE LISTING

<110> KYOWA HAKKO KOGYO CO., LTD

<120> Novel Transaldolase

<130> 00005.001198

<140> US/10/088,594

<141> 2002-03-21

<150> JP 99/266548

<151> 1999-09-21

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<170> PatentIn Ver. 2.0

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PCT10

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2 <110> APPLICANT: KYOWA HAKKO KOGYO CO., LTD
W--> 3 <120> TITLE OF INVENTION: Novel Transaldolase
W--> 4 <130> FILE REFERENCE: 00005.001198
W--> 5 <140> CURRENT APPLICATION NUMBER: US/10/088,594A
C--> 6 <141> CURRENT FILING DATE: 2002-06-11
7 <150> PRIOR APPLICATION NUMBER: JP 99/266548
8 <151> PRIOR FILING DATE: 1999-09-21
W--> 9 <160> NUMBER OF SEQ ID: 3
10 <170> SOFTWARE: PatentIn Ver. 2.0
W--> 11 <210> SEQ ID NO: 1
12 <211> LENGTH: 1080
13 <212> TYPE: DNA
14 <213> ORGANISM: Corynebacterium glutamicum ATCC31388
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18 1 5 10 15
19 gac gac ctc tcc cgc gag cgc att act tcc ggc aat ctc agc cag gtt 96
20 Asp Asp Leu Ser Arg Glu Arg Ile Thr Ser Gly Asn Leu Ser Gln Val
21 20 25 30
22 att gag gaa aag tct gta gtc ggt gtc acc acc aac cca gct att ttc 144
23 Ile Glu Glu Lys Ser Val Val Gly Val Thr Thr Asn Pro Ala Ile Phe
24 35 40 45
25 gca gca gca atg tcc aag ggc gat tcc tac gac gct cag atc gca gag 192
26 Ala Ala Ala Met Ser Lys Gly Asp Ser Tyr Asp Ala Gln Ile Ala Glu
27 50 55 60
28 ctc aag gcc gct ggc gca tct gtt gac cag gct gtt tac gcc atg agc 240
29 Leu Lys Ala Ala Gly Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser
30 65 70 75 80
31 atc gac gat gtt cgc aat gct tgt gat ctg ttc acc ggc atc ttc gag 288
32 Ile Asp Asp Val Arg Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu
33 85 90 95
34 tcc tcc aac ggc tac gac ggc cgc gtg tcc atc gag gtt gac cca cgt 336
35 Ser Ser Asn Gly Tyr Asp Gly Arg Val Ser Ile Glu Val Asp Pro Arg
36 100 105 110
37 atc tct gct gac cgc gac gca acc ctg gct cag gcc aag gag ctg tgg 384
38 Ile Ser Ala Asp Arg Asp Ala Thr Leu Ala Gln Ala Lys Glu Leu Trp
39 115 120 125
40 gca aag gtt gat cgt cca aac gtc atg atc aag atc cct gca acc cca 432
41 Ala Lys Val Asp Arg Pro Asn Val Met Ile Lys Ile Pro Ala Thr Pro
42 130 135 140
43 ggt tct ttg cca gca atc acc gac gct ttg gct gag ggc atc agc gtt 480
44 Gly Ser Leu Pro Ala Ile Thr Asp Ala Leu Ala Glu Gly Ile Ser Val

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RAW SEQUENCE LISTING

DATE: 07/22/2002

PATENT APPLICATION: US/10/088,594A

TIME: 14:12:56

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48          165          170          175
49 gcg tac atc gag gga atc aag cag gca gct gca aac ggc cac gac gta 576
50 Ala Tyr Ile Glu Gly Ile Lys Gln Ala Ala Ala Asn Gly His Asp Val
51          180          185          190
52 tcc aag atc cac tct gtg gct tcc ttc ttc gtc tcc cgc gtc gac gtt 624
53 Ser Lys Ile His Ser Val Ala Ser Phe Phe Val Ser Arg Val Asp Val
54          195          200          205
55 gag atc gac aag cgc ctc gag gca atc gga tcc gat gag gct ttg gct 672
56 Glu Ile Asp Lys Arg Leu Glu Ala Ile Gly Ser Asp Glu Ala Leu Ala
57          210          215          220
58 ctg cgc ggc aag gca ggc gtt gcc aac gct cag cgc gct tac gct gtg 720
59 Leu Arg Gly Lys Ala Gly Val Ala Asn Ala Gln Arg Ala Tyr Ala Val
60 225          230          235          240
61 tac aag gag ctt ttc gac gcc gcc gag ctg cct gaa ggt gcc aac act 768
62 Tyr Lys Glu Leu Phe Asp Ala Ala Glu Leu Pro Glu Gly Ala Asn Thr
63          245          250          255
64 cag cgc cca ctg tgg gca tcc acc ggc gtg aag aac cct gcg tac gct 816
65 Gln Arg Pro Leu Trp Ala Ser Thr Gly Val Lys Asn Pro Ala Tyr Ala
66          260          265          270
67 gca act ctt tac gtt tcc gag ctg gct ggt cca aac acc gtc aac acc 864
68 Ala Thr Leu Tyr Val Ser Glu Leu Ala Gly Pro Asn Thr Val Asn Thr
69          275          280          285
70 atg cca gaa ggc acc atc gac gct gtt ctg gaa ctg ggc aac ctg cac 912
71 Met Pro Glu Gly Thr Ile Asp Ala Val Leu Glu Leu Gly Asn Leu His
72          290          295          300
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74 Gly Asp Thr Leu Ser Asn Ser Ala Ala Glu Ala Asp Ala Val Phe Ser
75 305          310          315          320
76 cag ctt gag gct ctg ggc gtt gac ttg gca gat gtc ttc cag gtc ctg 1008
77 Gln Leu Glu Ala Leu Gly Val Asp Leu Ala Asp Val Phe Gln Val Leu
78          325          330          335
79 gag acc gag ggt gtg gac aag ttt gtt gct tct tgg agc gaa ctg ctt 1056
80 Glu Thr Glu Gly Val Asp Lys Phe Val Ala Ser Trp Ser Glu Leu Leu
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85 <210> SEQ ID NO: 2

86 <211> LENGTH: 1080

87 <212> TYPE: DNA

88 <213> ORGANISM: Corynebacterium glutamicum ATCC31388

W--> 89 <400> SEQUENCE: 2

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92 gtcaccacca acccagctat ttctgcagca gcaatgtcca agggcgattc ctacgacgct 180
93 cagatcgag agctcaaggc cgctggcgca tctgttgacc aggctgttta cgccatgagc 240

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PATENT APPLICATION: US/10/088,594A

TIME: 14:12:56

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 96 ctggctcagg ccaaggagct gtgggcaaag gttgatcgtc caaacgtcat gatcaagatc 420
 97 cctgcaaccc caggttcttt gccagcaatc accgacgctt tggctgaggg catcagcgtt 480
 98 aacgtcacct tgatcttctc cgttgctcgc taccgcgagg tcatcgctgc gtacatcgag 540
 99 ggaatcaagc aggcagctgc aaacggccac gacgtatcca agatccactc tgtggcttcc 600
 100 ttcttcgtct cccgcgtcga cgttgagatc gacaagcgcc tcgaggcaat cggatccgat 660
 101 gaggctttgg ctctgcgcgg caaggcaggc gttgccaacg ctacgcgcgc ttacgtctgtg 720
 102 tacaaggagc ttttcgacgc cgccgagctg cctgaagggtg ccaacactca gcgcccactg 780
 103 tgggcatcca ccggcgtgaa gaacctgcg tacgctgcaa ctctttacgt ttccgagctg 840
 104 gctggtccaa acaccgtcaa caccatgcc gaaggacca tcgacgctgt tctggaactg 900
 105 ggcaacctgc acggtgacac cctgtccaac tccgcggcag aagctgacgc tgtgttctcc 960
 106 cagcttgagg ctctgggcgt tgacttgga gatgtcttcc aggtcctgga gaccgaggt 1020
 107 gtggacaagt ttgttgcttc ttggagcgaa ctgcttgagt ccatggaagc tcgcctgaag 1080

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109 <211> LENGTH: 4108

110 <212> TYPE: DNA

111 <213> ORGANISM: Corynebacterium glutamicum ATCC31388

113 <220> FEATURE:

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117 <220> FEATURE:

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119 <222> LOCATION: (2643)..(3722)

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 123 ctacaaaagc ccacgtcaca gctcccagac ttaagattgg tcacaccttt gacacatttg 180
 124 aaccacagtt gggtataaaa tgggttcaac atcactatgg ttagagggtg tgacgggtca 240
 125 gattaagcaa agactacttt cggggtagat cacctttgcc aaatttgaat caattaacct 300
 126 aagtcgtaga tctgatcatc ggatctaacg aaaacgaacc aaaactttgg tcccggttta 360
 127 acccaggaag ga atg acc acc ttg acg ctg tca cct gaa ctt cag gcg ctc 411
 128 Met Thr Thr Leu Thr Leu Ser Pro Glu Leu Gln Ala Leu
 129 1 5 10
 130 act gta cgc aat tac ccc tct gat tgg tcc gat gtg gac acc aag gct 459
 131 Thr Val Arg Asn Tyr Pro Ser Asp Trp Ser Asp Val Asp Thr Lys Ala
 132 15 20 25
 133 gta gac act gtt cgt gtc ctc gct gca gac gct gta gaa aac tgt ggc 507
 134 Val Asp Thr Val Arg Val Leu Ala Ala Asp Ala Val Glu Asn Cys Gly
 135 30 35 40 45
 136 tcc ggc cac cca ggc acc gca atg agc ctg gct ccc ctt gca tac acc 555
 137 Ser Gly His Pro Gly Thr Ala Met Ser Leu Ala Pro Leu Ala Tyr Thr
 138 50 55 60
 139 ttg tac cag cgg gtt atg aac gta gat cca cag gac acc aac tgg gca 603
 140 Leu Tyr Gln Arg Val Met Asn Val Asp Pro Gln Asp Thr Asn Trp Ala
 141 65 70 75
 142 ggc cgt gac cgc ttc gtt ctt tct tgt ggc cac tcc tct ttg acc cag 651
 143 Gly Arg Asp Arg Phe Val Leu Ser Cys Gly His Ser Ser Leu Thr Gln
 144 80 85 90

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147 95 100 105
148 aag gct ctg cgc acc tgg gat tcc ttg acc cca gga cac cct gag tac 747
149 Lys Ala Leu Arg Thr Trp Asp Ser Leu Thr Pro Gly His Pro Glu Tyr
150 110 115 120 125
151 cgc cac acc aag ggc gtt gag atc acc act ggc cct ctt ggc cag ggt 795
152 Arg His Thr Lys Gly Val Glu Ile Thr Thr Gly Pro Leu Gly Gln Gly
153 130 135 140
154 ctt gca tct gca gtt ggt atg gcc atg gct gct cgt cgt gag cgt ggc 843
155 Leu Ala Ser Ala Val Gly Met Ala Met Ala Ala Arg Arg Glu Arg Gly
156 145 150 155
157 cta ttc gac cca acc gct gct gag ggc gaa tcc cca ttc gac cac cac 891
158 Leu Phe Asp Pro Thr Ala Ala Glu Gly Glu Ser Pro Phe Asp His His
159 160 165 170
160 atc tac gtc att gct tct gat ggt gac ctg cag gaa ggt gtc acc tct 939
161 Ile Tyr Val Ile Ala Ser Asp Gly Asp Leu Gln Glu Gly Val Thr Ser
162 175 180 185
163 gag gca tcc tcc atc gct ggc acc cag cag ctg ggc aac ctc atc gtg 987
164 Glu Ala Ser Ser Ile Ala Gly Thr Gln Gln Leu Gly Asn Leu Ile Val
165 190 195 200 205
166 ttc tgg gat gac aac cgc atc tcc atc gaa gac aac act gag atc gct 1035
167 Phe Trp Asp Asp Asn Arg Ile Ser Ile Glu Asp Asn Thr Glu Ile Ala
168 210 215 220
169 ttc aac gag gac gtt gtt gct cgt tac aag gct tac ggc tgg cag acc 1083
170 Phe Asn Glu Asp Val Val Ala Arg Tyr Lys Ala Tyr Gly Trp Gln Thr
171 225 230 235
172 att gag gtt gag gct ggc gag gac gtt gca gca atc gaa gct gca gtg 1131
173 Ile Glu Val Glu Ala Gly Glu Asp Val Ala Ala Ile Glu Ala Ala Val
174 240 245 250
175 gct gag gct aag aag gac acc aag cga cct acc ttc atc cgc gtt cgc 1179
176 Ala Glu Ala Lys Lys Asp Thr Lys Arg Pro Thr Phe Ile Arg Val Arg
177 255 260 265
178 acc atc atc ggc ttc cca gct cca acc atg atg aac acc ggt gct gtg 1227
179 Thr Ile Ile Gly Phe Pro Ala Pro Thr Met Met Asn Thr Gly Ala Val
180 270 275 280 285
181 cac ggt gct gct ctt ggc gca gct gag gtt gca gca acc aag act gag 1275
182 His Gly Ala Ala Leu Gly Ala Ala Glu Val Ala Ala Thr Lys Thr Glu
183 290 295 300
184 ctt gga ttc gat cct gag gct cac ttc gcg atc gac gat gag gtt atc 1323
185 Leu Gly Phe Asp Pro Glu Ala His Phe Ala Ile Asp Asp Glu Val Ile
186 305 310 315
187 gct cac acc cgc tcc ctc gca gag cgc gct gca cag aag aag gct gca 1371
188 Ala His Thr Arg Ser Leu Ala Glu Arg Ala Ala Gln Lys Lys Ala Ala
189 320 325 330
190 tgg cag gtc aag ttc gat gag tgg gca gct gcc aac cct gag aac aag 1419
191 Trp Gln Val Lys Phe Asp Glu Trp Ala Ala Ala Asn Pro Glu Asn Lys
192 335 340 345
193 gct ctg ttc gat cgc ctg aac tcc cgt gag ctt cca gcg ggc tac gct 1467

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198          370          375          380
199 aag gct tcc gag gct gca ctt cag gca ctg ggc aag acc ctt cct gag 1563
200 Lys Ala Ser Glu Ala Ala Leu Gln Ala Leu Gly Lys Thr Leu Pro Glu
201          385          390          395
202 ctg tgg ggc ggt tcc gct gac ctc gca ggt tcc aac aac acc gtg atc 1611
203 Leu Trp Gly Gly Ser Ala Asp Leu Ala Gly Ser Asn Asn Thr Val Ile
204          400          405          410
205 aag ggc tcc cct tcc ttc ggc cct gag tcc atc tcc acc gag acc tgg 1659
206 Lys Gly Ser Pro Ser Phe Gly Pro Glu Ser Ile Ser Thr Glu Thr Trp
207          415          420          425
208 tct gct gag cct tac ggc cgt aac ctg cac ttc ggt atc cgt gag cac 1707
209 Ser Ala Glu Pro Tyr Gly Arg Asn Leu His Phe Gly Ile Arg Glu His
210 430          435          440          445
211 gct atg gga tcc atc ctc aac ggc att tcc ctc cac ggt ggc acc cgc 1755
212 Ala Met Gly Ser Ile Leu Asn Gly Ile Ser Leu His Gly Gly Thr Arg
213          450          455          460
214 cca tac ggt gga acc ttc ctc atc ttc tcc gac tac atg cgt cct gca 1803
215 Pro Tyr Gly Gly Thr Phe Leu Ile Phe Ser Asp Tyr Met Arg Pro Ala
216          465          470          475
217 gtt cgt ctt gca gct ctc atg gag acc gac gct tac tac gtc tgg acc 1851
218 Val Arg Leu Ala Ala Leu Met Glu Thr Asp Ala Tyr Tyr Val Trp Thr
219          480          485          490
220 cac gac tcc atc ggt ctg ggc gaa gat ggc cca acc cac cag cct gtt 1899
221 His Asp Ser Ile Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val
222          495          500          505
223 gaa acc ttg gct gcg ctg cgc gcc atc cca ggt ctg tcc gtc ctg cgt 1947
224 Glu Thr Leu Ala Ala Leu Arg Ala Ile Pro Gly Leu Ser Val Leu Arg
225 510          515          520          525
226 cct gca gat gcg aat gag acc gcc cag gct tgg gct gca gca ctt gag 1995
227 Pro Ala Asp Ala Asn Glu Thr Ala Gln Ala Trp Ala Ala Ala Leu Glu
228          530          535          540
229 tac aag gaa ggc cct aag ggt ctt gca ctg acc cgc cag aac gtt cct 2043
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231          545          550          555
232 gtt ctg gaa ggc acc aag gag aag gct gct gaa ggc gtt cgc cgc ggt 2091
233 Val Leu Glu Gly Thr Lys Glu Lys Ala Ala Glu Gly Val Arg Arg Gly
234          560          565          570
235 ggc tac gtc ctg gtt gag ggt tcc aag gaa acc cca gat gtg atc ctc 2139
236 Gly Tyr Val Leu Val Glu Gly Ser Lys Glu Thr Pro Asp Val Ile Leu
237          575          580          585
238 atg ggc tcc ggc tcc gag gtt cag ctt gca gtt aac gct gcg aaa gct 2187
239 Met Gly Ser Gly Ser Glu Val Gln Leu Ala Val Asn Ala Ala Lys Ala
240 590          595          600          605
241 ctg gaa gct gag ggc gtt gca gct cgc gtt gtt tca gtt cct tgc atg 2235
242 Leu Glu Ala Glu Gly Val Ala Ala Arg Val Val Ser Val Pro Cys Met

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VERIFICATION SUMMARY

DATE: 07/22/2002

PATENT APPLICATION: US/10/088,594A

TIME: 14:12:57

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